

GENETIC VARIABILITY OF HORSESHOE CRAB,  
*Tachypleus gigas* (Müller) POPULATIONS FROM  
TANJUNG DAWAI, KEDAH AND CHERATING,  
PAHANG

SHAZANI BIN SARIJAN

MASTER OF SCIENCE  
UNIVERSITI MALAYSIA TERENGGANU  
MALAYSIA

2011

0/0 7831

1100083458

Perpustakaan Sultanah Nur Zahirah  
Universiti Malaysia Terengganu (UMT)



tesis  
QL 447.7 .S5 2011



1100083458  
Genetic variability of horseshoe crab, tachypleus gigas (muller)  
populations from Tanjung Dawai, Kedah and Cherating, Pahang  
/ Shazani Sarijan.

PERPUSTAKAAN SULTANAH NUR ZAHIRAH  
UNIVERSITI MALAYSIA TERENGGANU (UMT)  
21030 KUALA TERENGGANU

1100083458

|            |  |  |
|------------|--|--|
| 1100083458 |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |
|            |  |  |

Lihat sebelah

HAK MILIK  
PERPUSTAKAAN SULTANAH NUR ZAHIRAH UMT

**GENETIC VARIABILITY OF HORSESHOE CRAB, *Tachypleus gigas*  
(Müller) POPULATIONS FROM TANJUNG DAWAI, KEDAH AND  
CHERATING, PAHANG**

**SHAZANI BIN SARIJAN**

**Thesis Submitted in Fulfillment of the Requirement  
for the Degree of Master of Science in the  
Faculty of Science and Technology  
Universiti Malaysia Terengganu**

**April 2011**

Abstract of thesis presented to the Senate of Universiti Malaysia Terengganu  
in fulfillment of the requirements for the degree of Master of Science

**GENETIC VARIABILITY OF HORSESHOE CRAB, *Tachypleus gigas*  
(Müller) POPULATIONS FROM TANJUNG DAWAI, KEDAH AND  
CHERATING, PAHANG**

**SHAZANI BIN SARIJAN**

**April 2011**

**Chairperson : Noraznawati Binti Ismail, Ph.D.**

**Faculty : Science and Technology**

In Malaysia, horseshoe crabs, *Tachypleus gigas* (Müller) have been investigated for their abundance and morphology but very little information on their population size and phylogeny. This study was conducted to investigate the genetic variability and structure of two Malaysian *T. gigas* populations: Cherating, Pahang and Tanjung Dawai, Kedah. Random amplified polymorphic DNA (RAPD) and 18S rRNA gene sequence analyses were utilized to determine polymorphisms in these populations. Information obtained from RAPD and 18S rRNA gene sequences were then used to assess the genetic variation of *T. gigas* by constructing a phylogenetic tree analyses and their DNA divergence. The percentage of polymorphic loci for the Cherating and the Tanjung Dawai populations were 83.33% and 44.44% respectively. Based on the UPGMA dendrogram, the two population samples were segregated into two distinct clusters for both groups. From 18S rRNA gene sequence analysis, the net nucleotide divergence among populations was -0.0073 indicating a low polymorphism. Total number of mutations in

Tanjung Dawai was higher than Cherating samples, which are 73 and 59, thus reveal the evolutionary in the genome of Malaysian *T. gigas*. The tree topology of both populations inferred using NJ method by comparing 1791 bp of partial 18S rRNA sequence. The tree revealed that the *T. gigas* haplotypes were clustered into seven clades, suggesting that they are genetically diverse among population's derived from a common ancestor.

Abstrak tesis yang dikemukakan kepada Senat Universiti Malaysia Terengganu sebagai memenuhi keperluan untuk ijazah Sarjana Sains.

**KEBOLEHUBAHAN GENETIK BELANGKAS, *Tachypleus gigas* (Müller)  
POPULASI DARI TANJUNG DAWAI, KEDAH DAN CHERATING,  
PAHANG**

**SHAZANI BIN SARIJAN**

**April 2011**

**Pengerusi : Noraznawati Binti Ismail, Ph.D.**

**Fakulti : Sains dan Teknologi**

Kajian terhadap belangkas, *Tachypleus gigas* (Müller) di Malaysia kebanyakannya berkisarkan taburan dan morfologi tetapi terlalu sedikit maklumat mengenai saiz populasi dan filogeni. Kajian ini dijalankan untuk menyiasat kebolehubahan genetik dan struktur bagi dua populasi terpilih *T. gigas* di Malaysia: Cherating, Pahang dan Tanjung Dawai, Kedah. Pengandaan rawak polimorfik DNA (RAPD) dan analisis jujukan gen 18S rRNA telah digunakan untuk penentuan polimorfisme bagi kedua-dua populasi. Maklumat yang didapati daripada RAPD dan jujukan gen 18S rRNA seterusnya digunakan untuk memperoleh variasi genetik *T. gigas* melalui membina pokok filogenetik dan kepelbagaian DNA. Peratusan polimorfik loki bagi populasi Cherating dan Tanjung Dawai adalah masing-masing 83.33% dan 44.44%. Berdasarkan dendogram UPGMA, populasi kajian telah terpisah kepada dua kumpulan yang sangat jelas. Bagi analisis jujukan gen 18S rRNA pula, kepelbagaian nukleotid bersih bagi kedua-dua populasi ialah -0.0073 menunjukkan polimorfisme yang sangat rendah.

Bilangan mutasi bagi populasi Tanjung Dawai lebih tinggi berbanding Cherating, masing-masing 73 dan 59, menunjukkan evolusi dalam genom *T. gigas*. Pokok topologi kedua-dua populasi telah dibina melalui kaedah Neighbour-joining (NJ) melalui perbandingan 1791 bp separuh jujukan 18S rRNA. Pokok ini menunjukkan haplotip *T. gigas* terbahagi kepada tujuh suku, mencadangkan bahawa *T. gigas* secara genetiknya bertabur antara populasi yang mana berasal dari keturunan yang sama.